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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB seq length: 0
DB seq length: 2000000000
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       90
90
89
88.5
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1: pir1:*
2: pir2:*
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4: pir4:*
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Match
       BLOSUM62
Gapop 10.0 ,
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286
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Copyright (c) 1993 - 2000 Comp
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F71859
T48189
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C84701
T13738
F86321
T05064
E84918
E84296
E86321
F96572
A86315
F85016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Search time 101.54 Seconds
(without alignments)
48.262 Million cell updates/sec
hypothetical prote hypothetical prote hypothetical prote protein F12M16.10 F2H15.19 protein F12H16.10 protein F12H16.10 protein protein F12H16.10 protein RING-H2 finger propopothetical protein RING-H2 finger pr
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hypothetical
F6A14.12 prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                   cical prote
protein -
                                                   A; Map position: 2
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Query Match

39.98;

Score 114;

DB 2;

Length 310;

RESULT 2  C84701  C94701  C94701  C94701  C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 0.2-Feb-2001 #sequence_revision 0.2-Feb-2001 #text C; Accession: C84701  R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M; KOO, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanak M; KOO, H.; Moffat, W.C.; White, O.; Elsen, J.A.; Salzber Nature 402, 761-768, 1999 A; Title: Sequence and analysis of chromosome 2 of the pl A; Reference number: A84420; MUID:20083487 A; Accession: C84701 A; Residues: 1-310 <stoo 2<="" a:2929840="" a;="" c;="" cross-references:="" gb:ae002093;="" genetics:="" map="" nid:g3582320;="" pidn:aac:="" position:="" th=""><th>Query Match 78.7%; Score 225; DB 2; Length Best Local Similarity 76.0%; Pred. No. 8.7e-20; Matches 38; Conservative 7; Mismatches 5; Indel  Qy 1 RALCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV  </th><th>SULT 1  0807  AF interacting protein - Fugu rubripes AF interacting protein - Fugu rubripes Species: Fugu rubripes Species: Fugu rubripes Species: Fugu rubripes Species: 730807  Accession: 730807  Cottage, A. J.; Clark, M.; Hawker, K.; Umrania, Y.; Whe BS Lett. 443, 370-374, 1999  Title: Three receptor genes for plasminogen related gratile: Three receptor genes for plasminogen related gratiles: Table 7000  Status: preliminary translated from GB/EMBL/DDBJ  Molecule type: DNA  Mesidues: 1-433 <cot> Cross-references: EMBL:AJ010317; NID:e1355235; PID:e13  Cross-references: EMBL:AJ010317; NID:e1355235; PID:e13  Gene: TRIP  Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2;  Gene: TRIP  Ouery Match  Dest Local Similarity 76.0%; Pred. No. 8.7e-20;  Matches 38; Conservative 7; Mismatches 5; I  1 RALCTICSDEFINHSDNAAMOCGHTEHIOCLIOSEFETALDSEFTORCE</cot></th><th>30 86.5 30.2 477 2 JE0343 31 86.5 30.2 609 2 A43906 32 86 30.1 407 2 G96835 33 86 30.1 1238 2 T15919 34 85.5 29.9 227 2 T00428 35 85.5 29.9 1610 2 T11681 36 85 29.7 204 2 G84530 37 85 29.7 343 2 H96703 38 85 29.7 362 2 G84526 40 84.5 29.5 325 2 T04066 40 84.5 29.5 325 2 T04065 41 84.5 29.5 324 2 T08729 42 84.5 29.5 334 2 T08729 43 84 29.4 610 2 T22687 44 84 29.4 610 2 T22687 45 84 29.4 801 4 TVHURE</th></stoo>	Query Match 78.7%; Score 225; DB 2; Length Best Local Similarity 76.0%; Pred. No. 8.7e-20; Matches 38; Conservative 7; Mismatches 5; Indel  Qy 1 RALCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV	SULT 1  0807  AF interacting protein - Fugu rubripes AF interacting protein - Fugu rubripes Species: Fugu rubripes Species: Fugu rubripes Species: Fugu rubripes Species: 730807  Accession: 730807  Cottage, A. J.; Clark, M.; Hawker, K.; Umrania, Y.; Whe BS Lett. 443, 370-374, 1999  Title: Three receptor genes for plasminogen related gratile: Three receptor genes for plasminogen related gratiles: Table 7000  Status: preliminary translated from GB/EMBL/DDBJ  Molecule type: DNA  Mesidues: 1-433 <cot> Cross-references: EMBL:AJ010317; NID:e1355235; PID:e13  Cross-references: EMBL:AJ010317; NID:e1355235; PID:e13  Gene: TRIP  Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2;  Gene: TRIP  Ouery Match  Dest Local Similarity 76.0%; Pred. No. 8.7e-20;  Matches 38; Conservative 7; Mismatches 5; I  1 RALCTICSDEFINHSDNAAMOCGHTEHIOCLIOSEFETALDSEFTORCE</cot>	30 86.5 30.2 477 2 JE0343 31 86.5 30.2 609 2 A43906 32 86 30.1 407 2 G96835 33 86 30.1 1238 2 T15919 34 85.5 29.9 227 2 T00428 35 85.5 29.9 1610 2 T11681 36 85 29.7 204 2 G84530 37 85 29.7 343 2 H96703 38 85 29.7 362 2 G84526 40 84.5 29.5 325 2 T04066 40 84.5 29.5 325 2 T04065 41 84.5 29.5 324 2 T08729 42 84.5 29.5 334 2 T08729 43 84 29.4 610 2 T22687 44 84 29.4 610 2 T22687 45 84 29.4 801 4 TVHURE
idopsis thaliana 01 #text_change 02-Feb-2001 Benito, M.I.; Town, C.D.; Fujii, C.Y.; Vanaken, S.E.; Umayam, L.; Tallon, Salzberg, S.L.; Fraser, C.M.; Venter f the plant Arabidopsis thaliana. f the plant Agspbs:GN00139	Length 433; Indels 0; Gaps 0; PQCRIQV 50	<pre>.ext_change 02-Sep-2000 Wheller, D.; Bishop, M.; Elgar, I growth factors in the genome of e1355237; PIDN:CAA09084.1 e1355237; PIDN:CAA09084.1</pre>	terf protein - rat nuclear phosphopro probable RING zinc hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable RING zinc probable RING zinc hypothetical prote finger protein hypothetical prote ret finger protein hypothetical prote transforming prote

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C;Date: Variation: R66321

C;Accession: R66321

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Derasen, N.F.; Hughes, B.; Huizar, L.

Rature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M. Roiney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                            C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Murphy, L.; Harris, D.; Barrell, B.

Submitted to the EMEL Data Library, April 1999
A; Description: Sequencing the distal X chromoso
A; Reference number: 217668
A; Accession: 711738
  Дb
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                                                                                                                                                                                                                                                                                                                                  A;Reference number: A86141;
A;Accession: F86321
A;Status: preliminary
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
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c;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13738
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                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-325 <STO>
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A; Note: EG:22E5.12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-158 <MUR>
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Matches
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Best Local
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                          CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
VCTICLEEFDDGRSIVTLPCGHEFDEECVLEWF - - VRSHVCPLCRLEL 321
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                                                                                                                     Similarity
                                                                                            Conservative
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                                                                                       Score 112; DB 2; L
Pred. No. 3.7e-06;
Pred. No. 3.7e-106;
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1; Mismatches 16;
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L.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tallon,
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            R; Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000
                                                                                     hypothetical protein F9G14.60 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #C;Accession: T48296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: At2g47700
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-324 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein At2g47700 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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E84918
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C; Superfamily: RING finger homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein M3E9.170 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
A;Reference number:
                                                                                                                                                                                      T48296
                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE002093; NID:g3738284; PIDN:AAC63626.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402, 761-768, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: cultivar Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: AL022223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-344 <BEV>
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Best Local
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                                                                                                                                                                                                                                                                                                                          4 CTIC--SDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
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                                                                                                                                                                                                                                                                                                                                                                           l Similarity
19; Conserv
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18; Conser
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                                                                                                                                                                                                                                                                                                                                                                                               35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%;
38.3%;
                                                                                                                                                                                                                                                                                                                                                                           6,
                                                                                                                                                                                                                                                                                                                                                                      Score 102; DB 2
Pred. No. 6e-05;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 103; DB 2; Length 344; Pred. No. 4.8e-05; Mismatches 19; Indels
                                                                                                           -ear cress)
20-Apr-2000 #text_change 02-Sep-2000
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March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 324;
                                                                                                                                                                                                                                                                                                                                                                           19;
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De Clerck,

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protein F12M16.10 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear coress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: F96572 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons R;Theologis, A.; Ecker, J.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallot ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.X.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
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C; Superfamily: RING finger homology
F; 201-251/Domain: RING finger homology <RRN>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <BEV>
A;Cross-references: EMBL:AL162973
A;Experimental source: cultivar Columbia; BAC clone F9G14
C;Genetics:
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A; Residues: 1-224 <STO>
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Best Local S
Matches 18
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 CTICLEEFNDGTKVMTLPCGHEFDDECVLTWFET--NHDCPLCRFKL 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 38.3
les 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:AE005172; NID:g6730708; PIDN:AAF27103.1; GSPDB:GN00141
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Pred. No. 6.8e-05;
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Pred. No. 7.5e-05;
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                                                                   H.; Tallon,
                                                                                                                                                                                                                                              O.; Alonso, Dewar, K.;
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ewar, K.;
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                                                                   C; Genetics:
                                                                                                                             A; Molecule type: DNA
A; Residues: 1-506 <S
                                                                                                                                                                                                             A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A; Reference number: A85001; MUID: 20083488
A; Accession: F85016
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                                       A; Gene: AT4g01270
                                                                                              A;Cross-references: GB:NC_001268; NID:g7267624; PIDN:CAB80936.1; GSPDB:GN00140
                                                                                                                                                                                    A; Status: preliminary
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y; Lin, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. a;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F2H15.19 protein - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001 C;Accession: A86315 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
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A;Accession: F96572
A;Status: preliminary
                                                    probable RING zinc finger protein [imported] - Arabidopsis thaliana
C;Speckes: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: F85016
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R; anonymous, The European Union Arabidopsis Genome Nature 402, 769-777, 1999
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A; Residues: 1-383 <S
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A; Gene: F12M16.10
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A; Residues: 1-524 <STO>
                                                                                                                                                                       F85016
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Best Local
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    4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47

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                                                                                                                                                                                                                                                                                335 CSICQDEYEREDEVGELNCGHSFHVHCVKQWL--SRKNACPVCK 376
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16; Conserv
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <ST0>
                                                                                                                                                                                                                                                                                                                                                                                                                          34.3%;
34.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98; DB 2;
Pred. No. 0.00021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 99; DB 2;
Pred. No. 0.00021;
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                          Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 383;
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                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                             Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPDB: GN00141
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                          The Cold
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A; Note: DKFZp761D081.1
C; Superfamily: RING finger homology
F; 81-131/Domain: RING finger homolo
                                                                                                                                                                                                                 A;Cross-references: EMBL:AL157474
A;Experimental source: adult amygdala; clone DKFZp761D081
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
T46904
                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZp761D081.1 - human C;Species: Homo sapiens (man) C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T5A14.7 (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: F96597
  γ
                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-137 <AAA>
                                                                                                                                                                                                                                                                                                                                                  R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Weil, B.; Wiemann, submitted to the Protein Sequence Database, February 2000 A;Reference number: Z24136 A;Accession: T46904
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
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F96597
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                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005173; NID:g4204263; PIDN:AAD10644.1; GSPDB:GN00141
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A; Residues: 1-351 <STO>
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                                                                   Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                             l Similarity
17; Conserv
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18; Conserv
                                                                                                                                                    RING finger homology <RRN>
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                                                                 32.9%;
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                                        Score 94; DB 2; Lo
Pred. No. 0.00026;
7; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6,
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Pred. No. 0.00055;
9; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95; DB 2;
Pred. No. 0.00046;
6; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                                                                 Length 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 506;
                                          Indels
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reasy, T.H.;
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Marziali,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Alonso,
ewar, K.;
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C;Accession, .....
R;Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, April 1997
submitted to the sequence of C. elegans cosm
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;Superfamily: RING finger homology
C;Keywords: transmembrane protein
F;10-26/Domain: transmembrane #status predicted
F;46-62/Domain: transmembrane #status predicted
                                         Ş
                                                                                                                                                                                              A; Map position: 1
A; Introns: 3/1; 27/3; 86/1; 154/1; 201/3; 240/3; 268/3; 297/3
                                                                                                                                                                                                                                                                                                                                                                                             A;Description: The sequence
A;Reference number: Z20044
A;Accession: T25524
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S66695
    밁
                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U97193; PIDN:AAB52442.1; GSPDB:GN00019; CESP:C06A5.
A;Experimental source: strain Bristol N2; clone C06A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;105-121/Domain: transmembrane #status predicted <TM3>F;144-160/Domain: transmembrane #status predicted <TM4>F;144-150/Domain: transmembrane #status predicted <TM4>F;185-201/Domain: transmembrane #status predicted <TM5>F;345-405/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-551 < HUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Hughes, B.; Pohl, T.M. submitted to the Protein Sequence Database, July 1996 A;Reference number: S66685 A;Accession: S66695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable membrane protein YOL013c - yeas
N;Alternate names: hypothetical protein
C;Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                   A;Gene:
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-408 <DAV>
                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C06A5.9 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SGD: HRD1
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Matches
                                                                                                              Query Match
Best Local Similarity
                                                                                           Matches
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22
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                           CTICSDFFDHSRDVA-AMDCGHTFHLQCL--IQSFETAPSRTCPQCRIQ 49
    CQVCYQPFNETTKLARSLHCGHTFCTECIRNVQNYGNSPHLECPTCRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTICLSILEEGEDVRRLPCMHLFHQVCVDQWLIT--NKKCPICRVDI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICTICMDELTHSPNQQTWKNKNKKPKRLPCGHILHLSCLKNWMER--SQTCPICRLPV
                                                                                         Conservative
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                                                                                                            32.3%;
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                                                                                       13;
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                                                                                                              Score 92.5; DB 2; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 2; Lo
Pred. No. 0.0012;
5; Mismatches 20;
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tein 02341
                                                                                         Mismatches
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••
                                                                                         Gaps
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T26069
hypothetical protein W02All.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C; Accession: T26069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Molecule type: mRNA
A:Residues: 1-263,'LK', 266-624 <BEZ>
A:Residues: 1-263,'LK', 266-624 <BEZ>
A:Cross-references: EMBL:L04190; NID:g213867; PID:g213868
C:Comment: This DNA-binding phosphoprotein is enriched in nuclei of adult brain cells C:Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
E:158-207/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable zinc-binding protein - Iberian ribbed newt C;Species: Pleurodeles waltlii (Iberian ribbed newt) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000 C;Accession: S28418; S29476
                                                                                                                                                                                                                                                                                                          A;Map position: 1
A;Introns: 58/3; 129/3; 361/3; 444/3
C;Superfamily: RING finger homology
F;429-479/Domain: RING finger homology <RRN>
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  hypothetical C; Species: A:
                                         RESULT
F71425
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                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-489 <WIL>
A; Cross-references: EMBL: Z82062;
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A; Accession: S29476
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A; Residues: 1-624 <BEL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Bellini, M.; Lacroix, J.C.; Gall, J.G. EMBO J. 12, 107-114, 1993
                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; White, S.
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Best I
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                                                                                                                                                                 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
                                                                                                                          CTVCLSSFEDGESTQKLRCNHVFHPECIYKWLDI--NKRCPMCREEI
al protein -
Arabidopsis
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Arabidopsis
thaliana (mo
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                                                                                                                                                                                                                                32.2%;
27.7%;
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  (mouse-ear
                                                                                                                                                                                                          Score 92; DB
Pred. No. 0.00
12; Mismatches
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Pred. No. 0.00
3; Mismatches
                     thaliana
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  cress)
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A; Variety: columbia
C; Date: 03-Aug-1998 +
C; Accession: F71425
R; Bevan M.; Bancroft
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A; Accession: F71425
A; Status: Trail 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein AT4905350 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C:Accession: C85067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; C.; Chalwatzis, N.
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                                                                                                                                                                                         RESULT
T51859
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C; Superfamily: Arabidopsis thaliana
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C;Superfamily: RING finger homology
F;278-329/Domain: RING finger homol
                 A; Title: Widespread occurrence of a highly A; Reference number: Z13771; MUID: 98452956
                                                                                                RING-H2 finger protein RHGla [imported] - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18 - Aug-2000 #sequence_revision 18 - Aug-2000 #text_change 18 - Aug-20 C;Accession: T51859
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A; Residues: 1-441 <BEV>
A; Reference number: A: Accession: T51859
                                                         R;Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; FEBS Lett. 436, 283-7, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: AT4g05350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;anonymous, The European Union Arabidopsis Genome Nature 402, 769-777, 1999
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                        157 CSICLESLYSGPKPRDYTRMTCSHVFHNGCLLEWLKR--KNTCPLCRTEI 204
                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                4 CTICSDFF---DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
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18; Conserv
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18; Conser
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Pred. No. 0.00
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Score 90.5; DB
Pred. No. 0.001;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical RING
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                                       conserved RING-H2
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د.
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                                     finger motif
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A;Map position: 3
A;Introns: 37/3; 68/3; 90/3; 143/3; 181/3
C;Superfamily: RING finger homology
F;165-215/Domain: RING finger homology <R
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-292 <QUE>
A;Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.140
A;Experimental source: cultivar Columbia; BAC clone T17F15
                                                                                                                                                                                                                                  submitted to the Protein S
A;Reference number: Z15793
A;Accession: T06684
                                                                                                                                                                                                                                                                                                      hypothetical protein T17F15.140 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000 C;Accession: T06684 R;Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolice
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A;Map pc
                                                                                                                        C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 02-Mar-2001 #sequence_revision
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A;Molecule type: mRNA
A;Residues: 1-190 <JEN2
                                                                                                   A; Gene:
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A; Residues: 1-367 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATSP:T17F15.140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                 Choisne, N.; Robert, C.; Brottier, he Protein Sequence Database, April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
finger homology
ING finger homol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 90; DB 2;
Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN: AAC69857.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 367;
                                                                                                                                                                                                                                                                                 P.; Wincker, P.; Cattolico, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                         L.; Artigo
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T25457
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C;Species: Torpedo californica (Pacific electric ray)
C;Date: 19-May-1989 #sequence_revision 12-Mar-1993 #text_change 01-Dec-2000
C;Accession: A28009; B60088; I50550; I50551
R;Carr, C.; McCourt, D.; Cohen, J.B.
Biochemistry 26, 7090-7102, 1987
A;Title: The 43-kilodalton protein of Torpedo nicotinic postsynaptic membranes: A;Reference number: A28009; MUID:88107644
A;Accession: A28009
                                                                                                   A; Molecule type: mRNA
A; ResIdues: 364-405 <BAL>
R; Frail, D. E.; Mudd, J.; Shah, V.; Carr, C.; Cohen, J.B.; Merlie,
Proc. Natl. Acad. Sci. U.S.A. 84, 6302-6306, 1987
A; Title: CDNAs for the postsynaptic 43 kDa protein of Torpedo elec
A; Reference number: I50550; MUID:87317641
A; Accession: I50550
                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-386,'D', 388-403,'T',405 <CA2>
R;Baldwin, T.J.; Theriot, J.A.; Yoshihara, C.M.; Burden, S.J.
Development 104, 557-564, 1988
A;Title: Regulation of transcript encoding the 43K subsynaptic protein during develop A;Reference number: A60088; MUID:90032364
A;Accession: B60088
                     A; Molecule type: mRNA
A; Residues: 'MGQDQTK', 1-354,'Y', 356-382 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 2
A;Introns: 64/3; 99/3; 165/1; 267/3; 350/2; 386/2
C;Superfamily: RING finger homology
F;188-238/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U80836; PIDN:AAB37893.1; GSPDB:GN00020; CESP:B0432.9
A;Experimental source: strain Bristol N2; clone B0432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-425 <HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: The sequence of C. elegans cosmid B0432 A; Reference number: Z20038
                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                       A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43K postsynaptic membrane protein - Pacific electric ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: B0432.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Henkhaus, J.; Wohldmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 CLICLEEFHIGHEVRGLPCAHNFHVECIDQWLRL--NVKCPRCRCSV 213
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16; Conserv
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  GB:J02952;
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34.0%;
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NID: g213240;
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Pred. No. 0.00
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
PIDN: AAA49282.1;
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0.0029;
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                                                                                                                                                         Torpedo electric
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PID: g213241
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RESULT 26
T51841
RING-H2 finger |
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T13027
RING-H2 finger protein RHAlb - Arabidopsis thaliana
N;Alternate names: protein FBL21.150
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 02-Sep-2000
C;Accession: T13027
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Banci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 364-405 <FR2>
A;Cross-references: GB:J02953; NID:g213242; PIDN:AAA49283.1; PID:g213243
C;Comment: This protein is present in the postsynaptic apparatus at equimolar amounts
C;Keywords: alternative splicing; cytoskeleton; membrane protein; phosphoprotein
                                                                                                                                                                                                                                                                                                                                             C;Accession: T51841
R;Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, FEBS Lett. 436, 283-7, 1998
A;Title: widespread occurrence of a highly conserved RI: A;Reference number: Z13771; MUID:98452956
A;Accession: T51841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RING-H2 finger protein RHAlb [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
C;Superfamily: RING finger homology
F;81-134/Domain: RING finger homology <RRN>
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A;Experimental source: cultivar Columbia; BAC clone F8L21
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A; Residues: 1-157 <BEV>
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A; Accession: T13027
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A;Experimental source: cultivar Columbia
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A; Residues: 1-157 <JEN>
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Matches 16
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Best Local
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Best Local
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          85
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                                     4 CTIC-SDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTVCLSDFVSDDKIRQLPKCGHVFHHRCLDRWIVDCNKITCPICR 129
       CTVCLSDFVSDDKIRQLPKCGHVFHHRCLDRWIVDCNKITCPICR 129
                                                                                                       18;
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16; Conservative
                                                                                                                              Similarity
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                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, Sequence Database, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.6%;
                                                                                                                           30.6%;
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Pred. No. 0.0018;
""matches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
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Pred. No. 0.0032;
9; Mismatches 15;
                                                                                                                         Score 87.5; DB 2
Pred. No. 0.0018;
                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             conserved RING-H2 zinc finger motif in
                                                                                                     22;
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probable RING zinc finger protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (C;Accession: A84849 (S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
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                                                                                                                                                                           A84849
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hypothetical protein T4C9.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000 C;Accession: T48129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AT4g12190 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001 C;Accession: C85130
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C85130
                                                                                                                                        A;Note: T4C9.30
C;Superfamily: Arabidopsis thaliana hypothetical RING
F;150-203/Domain: RING finger homology <RRN>
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C; Superfamily: Arabidopsis thaliana hypothetical RING
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A;Residues: 1-194 <STO>
A;Cross-references: GB:NC_001268; NID:g7267920; PIDN:CAB78262.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488
A;Accession: C85130
                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z24485
A; Accession: T48129
                                                                                                                                                                                                                                                                                                                                                                                                                 R; Bevan, M.; Peters, S.A.; van Staveren, submitted to the Protein Sequence Databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
                                                                                                                                                                                                             A; Introns:
                                                                                                                                                                                                                            A; Map position: 4
                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                      A; Experimental source:
                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-203 <BEV>
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                                      Query Match
Best Local S
Matches 17
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Best Local
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4 CTICSDFF----DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
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                                        17; Conservative
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                                                           30.6%;
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                                      Score 87.5; DB 2;
Pred. No. 0.0023;
8; Mismatches 20;
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Pred. No. 0.0022;
B; Mismatches 2
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June 1999
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                                                                               Length 203;
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                                          Indels
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154 CSICLESLYSGPKPRDITRMTCSHVFHNGCLLEWLKR--KNTCPLCRTEL 201

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nuclear phosphoprotein xnf7 - African clawed frog C;Specles: Kenopus laevis (African clawed frog) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 C;Accession: A43906; S27947 R;Reddy, B.A.; Kloc, M.; Etkin, L. Dev. Biol. 148, 107-116, 1991 A;Title: The cloning and characterization of a mate A;Reference number: A43906; MUID:92038424 A;Accession: A43906
                                                                              C;Superfamily: Xenopus nuclear phosphoprotein xnf7; C;Keywords: DNA binding; nucleus; phosphoprotein; zi F;141-190/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 402, 761-768, 1999
A;Title: Sequence and analy:
A;Reference number: 844420;
A;Accession: A84849
A;Status: preliminary
                                                                                                                                               C;Genetics:
A;Gene: xnf7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-477 <OGA>
C;Superfamily: rfp transforming protein; RING finger homology
E;12-71/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: JE0343
R;Ogawa, S.; Goto, W.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Muramatsu, M.; Inoue, B;Ochem. Biochem. Biophys. Res. Commun. 251, 515-519, 1998
A;Title: Molecular cloning of a novel RING finger-B box-coiled coil (RBCC) profile response number: JE0343; MUID:99011410
A;Accession: JE0343
A;Status: preliminary
                                                                                                                                                                                    A;Cross-references: EMBL:M63705; NID:g214914; A;Note: sequence extracted from NCBI backbone
                                                                                                                                                                                                                                 A; Residues: 1-609 < RED>
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jun-2000
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A; Residues: 1-425 <STO>
                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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Best Local S
Matches 18
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Matches 16; Conserv
Best Local Similarity
                   Query Match
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l Similarity 32.1%;
18; Conservative
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0; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                red. No. 0.007; Mismatches
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Score
Pred.
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Pred. No. 0.0044;
9; Mismatches 19;
86.5; DB 2;
No. 0.0081;
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18;
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                                                                                                                                                                                    PID:g214915
(NCBIN:64515,
                                                                                                                                                                                                                                                                                                                maternally expressed novel zinc finger
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908 CAVCLERMDDS--VLAILCNHSFHARCL----EQWADNTCPVCR

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probable RING zinc finger protein, 53384-54880 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: 696835
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Fille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Reference ininary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein EEED8.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tcC;Accession: T15919
                                                                                                                                                                                            A;Gene: CESP:EEED8.9.
A;Introns: 16/3; 60/3; 140/1; 192/3; 269/2; 402/2;
C;Superfamily: RING finger homology
F;904-950/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1238 <CHI>
A; Cross-references: EMBL: U23484; NID: g733597;
A; Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: The sequence of C. elegans cosmid EE
A;Reference number: 218428
A;Accession: T15919
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005173; NID:g6751714; PIDN:AAF27696.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, July 1995 A; Description: The sequence of C. elegans cos
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A; Residues: 1-407 <STO>
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CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
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                                                                       l Similarity
18; Conserv
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                                                                       Conservative
                                                                                           30.1%;
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                                                                    Score 86; DB 2; Pred. No. 0.018; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB 2;
Pred. No. 0.0065;
9; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                PID:g733606; PIDN:AAC46769.1;
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                                                                                                                     Length 1238;
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hypothetical protein SPBC21D10.09c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C;Accession: T11681
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z17313
A;Accession: T11681
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A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: G84916
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C;Superfamily: Arabidopsis hypothetical protein F19I3.22; RING finger homology
F;104-155/Domain: RING finger homology <RRN>
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A;Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence
                                                                                                                                                    C;Superfamily: RING finger homology F;1554-1609/Domain: RING finger homology <RRN>
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A; Residues: 1-227 <STO>
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A; Residues: 1-227 < ROU>
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A; Accession: T00428
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R; Rounsley, S.D.;
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Best Local Similarity
Matches 17; Conserv
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                        Score 85.5; DB 2;
Pred. No. 0.026;
5; Mismatches 22
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Pred. No. 0.0044;
8; Mismatches 2
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lon, L.
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ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Jenkins, J.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Rathors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A; Tuthe: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number; A86141; MUID:21016719
A; Accession: H96703
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable RING zinc finger protein T23K23.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Map position: 2
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C;Genetics:
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A; Residues: 1-204 <STO>
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A; Residues: 1-343 <S
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Best Local Similarity
Matches 16; Conserv
                                                                                                         Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                              Genetics:
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position: 1
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292 CCICLSSYEDGAELVSLPCNHHFHSTCIVKWLKM--NATCPLCKFNI 336
                                                 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
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                                                                                                                                                                                                                                                                                                                                     GB:AE005173; NID:g6553889; PIDN:AAF16555.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.7%;
34.0%;
                                                                                                                                   29.7%;
25.5%;
                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                         Score 85; DB 2;
Pred. No. 0.0074;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 85; DB 2;
Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                              DB 2; Length 343,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                           GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                            2
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                         1;
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38

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hypothetical protein F28M11.70 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) C; Species: Arabidopsis thaliana (Mouse-ear cress) C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 02-Sep-2000 C; Accession: T04065 R; Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, March 1999 A; Reference number: Z15184 A; Accession: T04065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T04066
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson,
submitted to the Protein Sequence Database, M
A;Reference number: 215184
A;Accession: T04066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene:
A;Map po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G84526
hypothetical protein At2g15260 [imported] - Arabidopsis thaliana
c;Species: Arabidopsis thaliana (mouse-ear cress)
c;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
c;Accession: G84526
c;Accession: G84526
A; Molecule type: DNA
A; Residues: 1-236 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: F28M11.80
C; Superfamily: RING finger homology
F;93-144/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                               망
                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-225 <BEV>
A; Cross references: EMBL: AL049487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F28M11.80 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 02-Sep-2000 C;Accession: T04066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                   T04065
                                                                                                                                                                                                                                                                                        RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 68/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: cultivar Columbia; BAC clone F28M11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:AE002093; NID:g4662636; PIDN:AAD26908.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-362 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A84420; A; Accession: G84526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e: At2g15260
position: 2
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                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                           4 CTICSDFFDHSRDVAAM-DCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LCTICSDFF----DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
                                                                                                                                                                                                                                                                                                                                                            CSVCLGDYQAEEKLQQMPSCGHTFHMECI--DLWLTSHTTCPLCRLSL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Database, March 1999
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32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 85; DB 2; Pred. No. 0.0077; Pred. No. 0.0077; 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 84.5; DB 2;
Pred. No. 0.0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                      Mewes, H.W.; Mayer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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